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BIOLOGICAL DISTANCE IN THE 5—11TH CENTURIES POPULATIONS USING NON-METRIC FREQUENCY DATA

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Abstract

A sample of 807 crania representing two 5—6th, ten 6—8th, one 9—10th, one 10th and two 10—11th century populations were scored for 42 non-metric cranial traits in order to generate biological distance between these groups, elucidate migration patterns, or show genetic differences among these populations. Standard biological distance statistics were used to show the divergence among these groups and numerical taxonometric computer programs were utilized to display the relevant associations within and among these populations. Population samples under study were checked for side, sex and age dimorphism and dependencies of the traits utilized. It was found that while many of the Avar populations grouped together very well, some of the 5—6th populations grouped more closely with the 10—11th centuries materials than they do with the 6—8th centuries (Avar period) material. Some of this may be dues to small sample sizes for some of the 10th century Hungarian Conquest material.

Key words: biological distance, non-metric traits, 5—11th centuries (Gepid, Avar, Hungarian Conquest, Arpadian Age)

Introduction

Our ability to analyse the skeletal remains of earlier human populations by the use of non-metric and numerical taxonometric statistics has, to a considerable degree, added to the existing anthropological method of morphological taxonomy and metric analysis. Indeed, the sensitivity of the non-metric analysis may be used in assigning an individual cranium to one of a number of ethnic groups (FINNEGAN and MCGUIRE, 1979; FINNEGAN and RUBISON, 1984), to help in the identification of basic demographic parameters used in establishing individual identity in modern forensic anthropology (FINNEGAN, 1977), or in delineating microevolutionary changes (JANTZ, 1970; ORTNER and CORRUCCINI, 1976). However, in the broader sense, non-metric analysis has been most often used in comparing various populations with respect to biological distance (see FINNEGAN and FAUST, 1974; FINNEGAN, 1978 for detailed references).

Some of the most interesting migration patterns have occurred in Central Europe during the first millennium A. D. Some of the migrations of this period have been suggested on the basis of skeletal morphological taxonomy and fewer by robust metric statistical techniques, but only six of the populations from the Carpathian Basin have been studied with respect to non-metric traits (FINNEGAN

and MARCSIK, 1979). The purpose of this paper is to report continued analysis of earlier Hungarian populations using non-metric traits and numerical taxonometric statistics.

Material and method

Crania of 411 males and 396 females, representing 16 samples, two Gepid (5—6th c.) samples, 10 Avar (6—8th c.) period and one 9—10th c., three Hungarian Conquest and Early Arpadian aged (10—11th c.) samples were used. All samples are stored in the Department of Anthropology, Attila József University, Szeged, Hungary. Specifies samples are presented by name, cite location, sample size and rough date in Table 1. These samples are further elaborated for physical anthropology by one or more of the following: BARTUCZ, 1936; KŐHEGYI and MARCSIK, 1971; LIPTÁK, 1983; LIPTÁK and MARCSIK, 1966; 1970; 1976; LIPTÁK and VÁMOS, 1969; LIPTÁK and VARGA, 1974; LOTTERHOF, 1971; MARCSIK, 1971; VÁMOS, 1973; WENGER, 1955.

Table 1. Sample names and references used in this analysis along with maximum sample sizes and rough age by century. Sample sizes approximate 2n for those traits with bilateral occurrence

Population Sample	Reference	Sample size (2n)	Rough age (cent.)
1. Kunszállás-Fülöpjakab	LIPTÁK—VARGA 1974	62	8th
2. Mélykút-Sáncdülő	MARCSIK 1971	68	6—7th
3. Debrecen-Árkus Homokbánya	(not elaborated)	44	8th
4. Madaras-Téglavető	LIPTÁK—MARCSIK 1976	98	8th
5. Szeged-Fehértó-A	LIPTÁK—VÁMOS 1969	200	8th
6. Szeged-Kundomb	LIPTÁK—MARCSIK 1966	162	8th
7. Szeged-Makkoserdő	VÁMOS 1973	160	8th
8. Sükösd-Ságod	KŐHEGYI—MARCSIK 1971	140	7—8th
9. Kiszombor-B(Gepid)	BARTUCZ 1936	88	5—6th
10. Szőreg-Téglagyár	(not elaborated)	72	5—6th
11. Szabadkígyós-Tangazdaság and others	LOTTERHOF 1971, LIPTÁK 1983	170	10—11th
12. Kiskörös-Város alatt	LIPTÁK 1983	178	8th
13. Szarvas-Kákapuszta	LIPTÁK—MARCSIK 1970	34	9—10th
14. Szentes-Kaján	WENGER 1955	82	7—8th
15. Szentes-Borbástanya	LIPTÁK 1983	18	10th
16. Kiszombor-B (Arpadian Age)	(not elaborated)	48	10—11th

Each cranium in each sample was scored by one of us (MF) for the 42 cranial non-metric traits following FINNEGAN and MARCSIK (1979), which can be used for reference. Seven of these traits are expressed only along the mid-sagittal plane and sample size is therefore dependent on the number of crania studied. The remaining 35 traits have the possibility of bilateral expression and the sample size for these traits is limited to the number of sides of crania or approximately twice the number of crania. Each population sample was checked for age dependency and side and sex dimorphism utilizing the theta derived (ΘX^2) statistic whose distribution is very nearly the same as the standard X^2, with one degree of freedom.

$$\Theta X^2 = \frac{(\Theta_{1i} - \Theta_{2i})^2}{1/n_{1i} + 1/n_{2i}}$$

The Grewal-Smith statistic (mean measure of divergence (MMD), see FINNEGAN and COOPRIDER, 1978), was used to generate all between sample distance measures based on the transformed frequencies of the observed non-metric traits:

$$MMD = \sum_{i=1}^{R} [(\Theta_{1i} - \Theta_{2i})^2 - (1/n_{1i} + 1/n_{2i})]/R$$

Where $\Theta_{1i} = \arcsin(1 - 2P_{1i})$,
P_{1i} = frequency of the ith trait in the sample 1,
N_{1i} = total sides or total crania in sample 1,
i = trait number under summation,
R = number of traits for a particular data set.

While the MMD distance are complete in themselves, further testing and geographic representation of the population samples are possible with numerical taxonometric statistics (SOKAL and SNEATH 1963; ROHLF, 1967; ROHLF et al, 1974). In this analysis the 16 dimensional matrix was subjected to a sequential agglomerative hierarchial cluster analysis (TAXON) using the unweighted pair-group method with arithmetic averages (UPGMA) using low values for similarity or least biological distance. A cophonetic value metrix was generated and compared to the original distance matrix for conguerence, which can be displayed as a bivariate scatter plot and can also be expressed as a correlation.

Results

While correlation analysis showed some age dependency, standard chi square analysis between younger and older crania showed the few significant differences to be less than chance expectation. Additionally, immature individuals had not been used in this analysis and the age range was generally between 20 and 60 years. Side to side differences were significant (ΘX^2) at or above .05 level in 3.72% of the male samples and 4.16% in female samples. While these differences are below chance expectation it should be noted that trait expression in a sample is rarely symmetrical and that these asymmetries can be used in ethnic identification of individual crania (FINNEGAN and MCGUIRE, 1979; FINNEGAN and RUBISON, 1984). In this analysis we have pooled left and right sides.

Sex differences were more pronounced generating 8.33% significant differences between males and females on each of the left and right sides comparisons. This exceeds chance expectation and some of these differences were significant at the .01 level or higher. However, these significant differences are more or less evenly distributed across the 42 traits with both sex comparisons by side, showing slightly more than 1 significant difference per trait. Similarly, most traits showed one or more significant sex differences across the 16 population samples treating left and right sides separately, suggesting some randomness to the distribution.

For analysis we have pooled our sides and sexes in generating our distance matrix for the following reasons: 1. the number of each sex is about equal in each population; 2. where significant sex differences occur we generally find them to be directional and similar in each population; 3. sex dimorphic traits have often proven to be the most important discriminators in showing population separation by principal component analysis (KELLOCK and PARSONS, 1979; FINNEGAN, 1972; BERRY, 1975; FINNEGAN, 1978; BERRY, 1979; FINNEGAN and MARCSIK, 1979).

The raw data for frequency and sample size are given in Tables 2 and 3. The

Table 2. Frequencies for each trait in each population sample used in this analysis with sides and sexes pooled.

CRANIAL NON-METRIC TRAITS:	HU 1	HU 2	HU 3	HU 4	HU 5	HU 6
1. HIGHEST NUCHAL LINE	.500	.391	.700	.511	.823	.642
2. CORONAL OSSICLES	.000	.000	.000	.011	.020	.037
3. OSSICLE AT BREGMA	.000	.000	.000	.021	.010	.000
4. SAGITTAL OSSICLES	.034	.000	.053	.021	.160	.037
5. OSSICLE AT LAMBDA	.033	.030	.200	.064	.204	.192
6. LAMBDOID OSSICLES	.204	.295	.406	.375	.469	.418
7. OS INCA	.000	.000	.000	.000	.000	.000
8. PARIETAL FOR.	.548	.603	.395	.559	.445	.542
9. PARIETAL NOTCH BONE	.100	.018	.000	.023	.116	.063
10. ASTERIONIC BONE	.000	.019	.000	.071	.060	.103
11. AUDITORY TORUS	.000	.000	.000	.000	.000	.000
12. MALAR TUBERCLE	.088	.000	.000	.000	.000	.000
13. OS JAPON	.019	.000	.000	.000	.010	.006
14. PTERION FORM	.056	.020	.000	.012	.020	.057
15. EPITERIC BONE	.056	.021	.200	.128	.278	.190
16. INFRA-ORBITAL FOR.	.021	.027	.000	.050	.060	.044
17. SUPRA-ORBITAL FOR.	.458	.263	.216	.280	.151	.167
18. FRONTAL FOR. PRESENT	.390	.179	.108	.228	.156	.222
19. METOPIC SUTURE	.097	.000	.050	.022	.102	.064
20. MANDIBULAR FOR.	.000	.019	.043	.058	.056	.039
21. MYLOHYOID GROOVE	.054	.035	.000	.011	.030	.033
22. MANDIBULAR TORUS	.288	.000	.000	.065	.056	.058
23. MENTAL FORAMEN	.119	.051	.065	.056	.081	.045
24. PALATINE TORUS	.148	.045	.071	.119	.162	.300
25. ACC. LES PALATE FOR.	.419	.433	.269	.228	.236	.483
26. FOR. OF VESALIUS	.325	.200	.182	.164	.218	.161
27. FOR. OVALE	.164	.067	.208	.059	.046	.053
28. FOR. SPINOSUM	.179	.227	.360	.165	.093	.171
29. FOR. OF HUSCHKE	.230	.220	.200	.250	.060	.043
30. CONDYLAR FACET	.000	.044	.000	.000	.026	.042
31. POST. CONDY. FOR.	.400	.490	.759	.711	.618	.599
32. PRECONDY. TUBERCLE	.040	.036	.000	.068	.080	.110
33. ANTERIOR CONDY. FOR.	.184	.115	.233	.115	.216	.167
34. MASTOID FOR.	.839	.725	.765	.837	.749	.850
35. MASTOID FOR. EXSUT.	.304	.196	.382	.244	.256	.183
36. PARAMASTOID PROCESS	.917	.829	.999	.919	.881	.852
37. DIGASTRIC GROOVE	.310	.264	.242	.267	.311	.281
38. STYLOMASTOID FOR.	.016	.000	.000	.000	.000	.000
39. ZYGO-MAX. TUBEROS.	.582	.442	.423	.506	.707	.732
40. ZYGO-FACIAL FOR.	.113	.354	.100	.198	.242	.217
41. ANT. ETH. FOR. EX.	.462	.619	.889	.370	.185	.200
42. POST. ETHMOID FOR.	.053	.263	.000	.160	.199	.083

HU 7	HU 8	HU 9	HU 10	HU 11	HU 12	HU 13	HU 14	HU 15	HU 16
.713	.692	.892	.686	.748	.551	.571	.688	.813	.933
.006	.000	.023	.031	.028	.028	.030	.050	.000	.042
.000	.015	.000	.029	.000	.000	.000	.000	.000	.000
.123	.046	.025	.000	.055	.024	.000	.083	.000	.091
.351	.156	.098	.194	.247	.181	.143	.182	.375	.174
.518	.425	.300	.554	.552	.420	.500	.462	.438	.267
.000	.000	.000	.000	.000	.000	.000	.000	.000	.042
.462	.485	.536	.493	.451	.500	.500	.679	.625	.646
.130	.111	.153	.048	.087	.070	.133	.095	.125	.130
.187	.081	.024	.111	.136	.053	.148	.154	.188	.149
.000	.000	.000	.000	.000	.017	.067	.012	.000	.104
.032	.020	.100	.071	.034	.086	.100	.056	.188	.128
.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
.058	.017	.012	.000	.000	.006	.030	.012	.000	.000
.134	.168	.247	.152	.128	.161	.161	.206	.188	.256
.018	.037	.085	.000	.088	.023	.031	.026	.118	.000
.127	.158	.214	.085	.138	.226	.294	.222	.333	.104
.199	.114	.167	.155	.242	.109	.176	.232	.333	.152
.063	.086	.093	.056	.048	.067	.059	.146	.000	.083
.069	.052	.141	.082	.085	.047	.071	.086	.067	.146
.061	.061	.095	.021	.030	.094	.037	.089	.000	.104
.058	.054	.000	.000	.167	.064	.000	.067	.438	.083
.059	.046	.045	.019	.091	.045	.100	.016	.313	.042
.029	.051	.049	.143	.066	.140	.250	.243	.778	.522
.271	.151	.200	.273	.206	.174	.172	.194	.188	.273
.115	.196	.333	.171	.271	.064	.000	.116	.214	.152
.088	.067	.081	.116	.028	.035	.034	.068	.063	.111
.115	.167	.137	.220	.096	.115	.107	.091	.000	.156
.131	.212	.081	.138	.156	.088	.033	.099	.000	.042
.025	.000	.000	.048	.000	.072	.000	.000	.000	.000
.598	.602	.658	.581	.644	.303	.286	.504	.688	.574
.044	.057	.000	.045	.000	.080	.125	.000	.000	.043
.183	.178	.253	.200	.163	.166	.097	.190	.125	.311
.897	.866	.901	.942	.905	.948	.000	.941	.938	.809
.375	.361	.444	.269	.250	.263	.464	.279	.125	.191
.912	.824	.781	.850	.765	.970	.966	.922	.875	.911
.224	.222	.253	.200	.207	.232	.276	.192	.125	.283
.013	.000	.000	.000	.000	.000	.000	.025	.000	.000
.350	.410	.284	.458	.370	.560	.412	.570	.611	.596
.192	.221	.165	.263	.142	.292	.030	.221	.176	.064
.388	.244	.132	.444	.406	.132	.167	.146	.286	.205
.512	.341	.185	.118	.185	.162	.120	.208	.000	.163

Table 3. Sample sizes for each trait in each population sample. Bilateral traits have the possibility of 2N, while midline traits have a maximum possibility of N, or the number of crania in the sample.

CRANIAL NON-METRIC TRAITS:	HU 1	HU 2	HU 3	HU 4	HU 5	HU 6
1. HIGHEST NUCHAL LINE	60.	64.	40.	88.	192.	151.
2. CORONAL OSSICLES	56.	59.	35.	94.	200.	160.
3. OSSICLE AT BREGMA	28.	29.	18.	47.	99.	81.
4. SAGITTAL OSSICLES	29.	32.	19.	47.	100.	81.
5. OSSICLE AT LAMBCA	30.	33.	20.	47.	98.	78.
6. LAMBDOIC OSSICLES	54.	61.	32.	88.	196.	153.
7. OS INCA	31.	33.	20.	46.	100.	78.
8. PARIETAL FORAMEN	62.	63.	38.	93.	200.	155.
9. PARIETAL NOTCH BONE	60.	56.	26.	86.	199.	159.
10. ASTERIONIC BONE	58.	53.	23.	84.	200.	155.
11. AUDITORY TORUS	61.	54.	32.	92.	200.	161.
12. MALAR TUBERCLE	57.	43.	34.	73.	200.	160.
13. OS JAPON	53.	42.	29.	81.	196.	157.
14. PTERION FORM	54.	49.	21.	86.	199.	158.
15. EPITERIC BONE	54.	47.	20.	86.	198.	158.
16. INFRA-ORBITAL FORAMEN	47.	37.	24.	60.	199.	159.
17. SUPRA-ORBITAL FORAMEN	59.	57.	37.	93.	199.	162.
18. FRONTAL FORAMEN	59.	56.	37.	92.	199.	162.
19. METOPIC SUTURE	31.	30.	20.	46.	98.	78.
20. MANDISULAR FORAMEN	56.	54.	21.	86.	197.	152.
21. MYLOHYOID GROOVE	56.	57.	20.	88.	198.	153.
22. MANDIBULAR TORUS	59.	59.	35.	92.	198.	156.
23. MENTAL FORAMEN	59.	59.	31.	90.	198.	155.
24. PALATINE TORUS	27.	22.	14.	42.	99.	80.
25. ACC. LES. PALATINE FOR.	43.	30.	26.	57.	191.	149.
26. FOR. OF VESALIUS	40.	25.	22.	67.	193.	143.
27. FORAMEN OVALE	55.	45.	24.	85.	197.	151.
28. FORAMEN SPINOSUM	56.	44.	25.	85.	193.	152.
29. FORAMEN OF HUSCHKE	61.	50.	30.	92.	199.	161.
30. CONDYLAR FACET	48.	45.	28.	78.	191.	142.
31. POST. CONDY. FOR.	45.	49.	29.	76.	191.	142.
32. PRECONDY. TUBERCLE	25.	28.	17.	44.	100.	73.
33. ANTERIOR CONDY. FOR.	49.	52.	30.	87.	199.	144.
34. MASTOID FORAMEN	56.	51.	34.	86.	195.	153.
35. MASTOID F. EXSUTURAL	56.	51.	34.	86.	195.	153.
36. PARAMASTOID PROCESS	48.	35.	15.	62.	193.	135.
37. DIGASTRIC GROOVE	58.	53.	33.	86.	196.	153.
38. STYLOMASTOID FORAMEN	61.	53.	27.	92.	198.	161.
39. ZYGO-MAX. TUBERCSITY	55.	43.	26.	77.	198.	157.
40. ZYGO-FACIAL FORAMEN	53.	48.	30.	86.	198.	157.
41. ANT. ETH. F. EXSUTURAL	26.	21.	9.	46.	157.	130.
42. POST. ETHMOID FORAMEN	38.	19.	10.	50.	171.	133.

HU 7	HU 8	HU 9	HU 10	HU 11	HU 12	HU 13	HU 14	HU 15	HU 16
136.	130.	74.	70.	143.	156.	28.	64.	16.	45.
156.	126.	86.	64.	141.	178.	33.	80.	18.	48.
78.	65.	42.	34.	73.	86.	17.	38.	9.	23.
73.	65.	40.	34.	73.	84.	15.	36.	7.	22.
74.	64.	41.	36.	73.	83.	14.	33.	8.	23.
139.	127.	80.	65.	134.	169.	24.	65.	16.	45.
76.	68.	43.	35.	81.	88.	14.	37.	8.	24.
156.	136.	84.	71.	153.	176.	28.	78.	16.	48.
146.	117.	85.	63.	138.	172.	30.	74.	16.	46.
134.	111.	84.	63.	132.	169.	27.	65.	16.	47.
151.	120.	87.	62.	156.	173.	30.	81.	18.	48.
124.	100.	80.	56.	117.	151.	30.	71.	16.	47.
125.	114.	80.	56.	118.	168.	33.	77.	17.	47.
139.	119.	86.	56.	141.	175.	33.	81.	18.	46.
134.	113.	77.	46.	117.	174.	31.	68.	16.	43.
114.	109.	71.	41.	102.	171.	32.	76.	17.	48.
157.	133.	84.	71.	152.	177.	34.	81.	18.	48.
156.	132.	84.	71.	153.	175.	34.	82.	18.	46.
80.	70.	43.	36.	83.	89.	17.	41.	9.	24.
130.	115.	85.	49.	129.	106.	28.	58.	15.	48.
132.	115.	84.	48.	132.	106.	27.	56.	15.	48.
137.	130.	88.	53.	144.	109.	28.	60.	16.	48.
136.	130.	88.	52.	143.	111.	30.	63.	16.	48.
69.	59.	41.	28.	61.	86.	16.	37.	9.	23.
96.	86.	60.	33.	68.	161.	29.	67.	16.	44.
96.	97.	72.	41.	85.	171.	28.	69.	14.	46.
125.	104.	74.	43.	106.	172.	29.	74.	16.	45.
131.	108.	73.	41.	115.	174.	28.	77.	16.	45.
153.	118.	86.	58.	154.	170.	30.	81.	18.	48.
121.	99.	75.	42.	99.	167.	29.	54.	15.	45.
117.	98.	73.	43.	104.	165.	28.	55.	16.	47.
68.	53.	39.	22.	50.	88.	16.	32.	8.	23.
126.	101.	75.	45.	104.	175.	31.	63.	16.	48.
136.	97.	81.	52.	116.	172.	28.	68.	16.	47.
136.	97.	81.	52.	116.	171.	28.	68.	16.	47.
102.	85.	64.	40.	85.	169.	29.	51.	16.	45.
147.	117.	83.	55.	150.	164.	29.	73.	16.	46.
152.	119.	87.	61.	157.	174.	30.	81.	18.	48.
123.	117.	81.	59.	119.	175.	34.	79.	18.	47.
125.	113.	79.	57.	120.	171.	33.	77.	17.	47.
85.	86.	53.	18.	64.	159.	30.	48.	14.	44.
84.	91.	54.	17.	65.	160.	25.	53.	15.	43.

mean measure of divergence among all populations, males and females, left and right sides all pooled, is given in Table 4. All between population differences are significant at the .05 level and most are significant are the .01 level. Figure 1 represents the 16 by 16 population clustered distance matrix as a phenogram, computed by the unweighted pair group method based on arithmetic averages. Low distance values were specified to indicate the corresponding distance similarities. When the cophonetic value matrix was plotted against the original distance matrix, little distortion was found in the bivariate plot of the two matrices and they produced a correlation of 0.777. While we belive this correlation is significant, SOKAL and DERISH (1988) (see also DERISH and SOKAL, 1988) suggests highly significant cophonetic correlations should be in the neighborhood of 0.85. Considering the size, spatial and temporal distribution of our population samples we feel the cophonetic correlations to be quite good.

Discussion

The distance phenograph (Figure 1) nicely divides into three major groups with four, more or less, single samples if we consider an identity level of 0.055. While this choice is somewhat arbitrary, it does fit the various time periods and allows some confidence in the phenogram and our overall analysis.

Group 1 is composed of Gepid samples, one middle and two late Avar period samples and the heterogeneous sample from the 10—11th century. Most of these samples fall within a 500 year time range and are distributed across southern Hungary.

Group 2 includes four samples, three representing the late Avar period and one from the Hungarian Conquest-Early Arpadian Age. Here the temporal range is about three centuries and the lowest biological distance is found between two late Avar period samples which are spatially separated by a few kilometers. The overall similarity in this group is somewhat greater than that found in group one, but it is composed of fewer samples with reduced temporal and spatial distributions.

Group 3 represents one late Avar and one 9—10th century samples from south central Hungary. We might have expected these population samples to have been part of group 2, expect for the fact, as noted by LIPTÁK (1983), that sample 12 shows a sex difference with respect to the proportion of Mongoloid morphological characters — females displaying more. As well, sample 13 shows a Europid-Mongoloid mix and may be one of the latest Avar period populations-possibly surviving into the 10th century (SZABÓ, 1966).

The remaining population samples are grouped above our arbitrary level of 0.055 and are not specific enough to be meaningful as a group. This is supported by the fact that sample 1 is a late Avar sample with a noticeable amount of Mongoloid morphological features, and is spatially distant from our other Avar period samples. Sample 2 is very early, possibly representing the „first wave" of Avar migration. As well, this sample represents two large families, rather than a random sample of a

Table 4. Measure of Divergence (biological distance) between population samples used in this study. All distance measures are significant ($p<.05$) and most are very significant ($p<.01$).

Population Sample	1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.	13.	14.	15.	16.
1. Kunszáll	.000															
2. Mélykút	.072	.000														
3. Árkus	.116	.085	.000													
4. Madaras	.051	.018	.066	.000												
5. Fehértó	.115	.117	.138	.045	.000											
6. Kundomb	.087	.082	.140	.034	.020	.000										
7. Makkoserdő	.131	.094	.142	.056	.053	.078	.000									
8. Sükösd	.088	.062	.116	.014	.030	.058	.014	.000								
9. Kiszombor	.125	.121	.143	.071	.062	.095	.068	.025	.000							
10. Szőreg	.111	.046	.060	.023	.053	.038	.040	.020	.049	.000						
11. Szabadka	.098	.094	.113	.033	.050	.068	.032	.019	.044	.033	.000					
12. Kiskörös	.099	.094	.165	.052	.055	.048	.063	.041	.081	.035	.074	.000				
13. Szarvas	.137	.145	.181	.076	.108	.080	.085	.072	.091	.052	.100	.019	.000			
14. Sz-Kaján	.095	.119	.151	.038	.035	.036	.039	.025	.039	.031	.031	.022	.039	.000		
15. Sz-Borbás	.150	.260	.246	.140	.137	.106	.203	.179	.180	.146	.095	.145	.137	.094	.000	
16. Kiszombor	.138	.188	.173	.100	.058	.062	.102	.081	.075	.067	.086	.077	.081	.026	.088	.000

larger population (FARKAS, LENGYEL and MARCSIK, 1971). Sample 3 represents a population geographically removed from southeastern Hungary. This sample was a priori chosen to serve as a control sample. Sample 15 represents a Hungarian Conquest single great family (LIPTÁK, 1983). As such, the variation in this sample may be reduced and, like sample 2, does not necessarily represent the larger population. This is also the smallest sample studied.

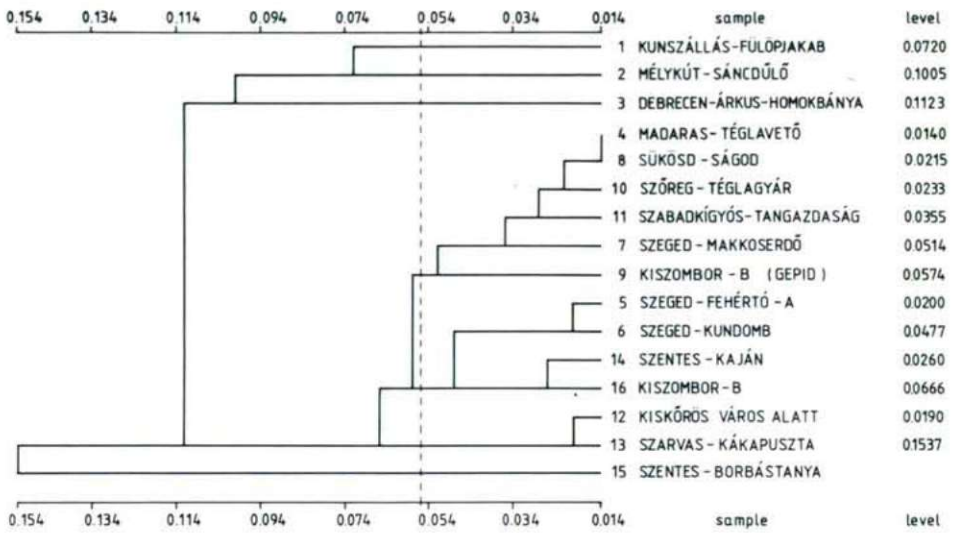

Fig. 1. A phenogram based on the clustered distance matrix (males and females; left and right sides pooled) using the unweighted pair-group method with arithmetic averages. Low values were specified to indicate corresponding distance similarities. Abscissa is scaled in relative population distances.

Admittedly, the cluster process in the numerical taxonometric system is somewhat artificial. For example, sample 8 generated a biological distance of 0.014 with both samples 4 and 7. The fact that the phenogram joins sample 8 with sample 4 is due to the fact that in the clustering process sample 4 is encountered and clustered before sample 7. Then, because of arithmetic averaging, all other values of samples 8 and 4 are averaged, including the value between samples 8 and 7. Nevertheless, sample 7 is clustered within the group containing samples 4 and 8. In addition, other transformations of the frequencies could have been used which may have altered the distance statistic, but here we used the transformation recommended by FINNEGAN and COOPRIDER (1978).

In this research we have shown the biological relationships among samples of earlier human populations, representing some of the Gepid tribes of the 5—6th centuries, the Avar period during the 6—8th centuries, and some Hungarian Conquest populations of the 10th and 11th centuries. While we can suggest general migration patterns in this broad region over time, the present analysis does not further identify or delimit time, direction or distance specifically. As our research

into population behavior in the Carpathian basin during the 5—11th centuries continues, and as the archaeology of these populations is explored in greater depth, we may be better able to identify and trace the migrations of earlier human populations in this area.

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